

1652

01/17/02

1600

RAW SEQUENCE LISTING

PARENT APPLICATION: US/09/722,602A

DATE: 01/03/2002

TIME: 13:02:00

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01032002\I722602A.raw

TECH CENTER 300 2800

RECEIVED

ENTERED

4 <110> APPLICANT: ARNOLD, Frances H.
 5 PETROUNIA, Ionna P.
 6 SUN, Lianhong
 8 <120> TITLE OF INVENTION: DIRECTED EVOLUTION OF OXIDASE ENZYMES
 11 <130> FILE REFERENCE: 9373/1G811US1
 13 <140> CURRENT APPLICATION NUMBER: 09/722,602A
 14 <141> CURRENT FILING DATE: 2000-11-27
 16 <150> PRIOR APPLICATION NUMBER: US 09/571,553
 17 <151> PRIOR FILING DATE: 2000-05-16
 19 <160> NUMBER OF SEQ ID NOS: 48
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Primer
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 35 <211> LENGTH: 33
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Primer
 42 <400> SEQUENCE: 2
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 48 <213> ORGANISM: Artificial Sequence
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Primer
 53 <400> SEQUENCE: 3
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 57 <211> LENGTH: 32
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Primer
 64 <400> SEQUENCE: 4
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 67 <210> SEQ ID NO: 5
 68 <211> LENGTH: 30
 69 <212> TYPE: DNA
 70 <213> ORGANISM: Artificial Sequence

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72 <220> FEATURE:
73 <223> OTHER INFORMATION: Primer
75 <400> SEQUENCE: 5
76 accatgattt cgaagtcggt accctcagca 30
78 <210> SEQ ID NO: 6
79 <211> LENGTH: 30
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Primer
86 <400> SEQUENCE: 6
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89 <210> SEQ ID NO: 7
90 <211> LENGTH: 30
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Primer
97 <400> SEQUENCE: 7
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100 <210> SEQ ID NO: 8
101 <211> LENGTH: 29
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Primer
108 <400> SEQUENCE: 8
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111 <210> SEQ ID NO: 9
112 <211> LENGTH: 30
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Primer
119 <400> SEQUENCE: 9
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122 <210> SEQ ID NO: 10
123 <211> LENGTH: 639
124 <212> TYPE: PRT
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Mutant 9.16.8D2 (N537D) of D. dendroides GaO
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132 1 5 10 15
133 Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
134 20 25 30
135 Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
136 35 40 45

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137 Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
138      50                      55                      60
139 Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
140 65                      70                      75                      80
141 Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
142                      85                      90                      95
143 Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
144      100                      105                      110
145 Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
146      115                      120                      125
147 Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
148      130                      135                      140
149 Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
150 145                      150                      155                      160
151 Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
152                      165                      170                      175
153 Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
154      180                      185                      190
155 Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
156      195                      200                      205
157 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
158      210                      215                      220
159 Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
160 225                      230                      235                      240
161 Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
162      245                      250                      255
163 Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
164      260                      265                      270
165 Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
166      275                      280                      285
167 Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
168      290                      295                      300
169 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
170 305                      310                      315                      320
171 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
172      325                      330                      335
173 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
174      340                      345                      350
175 Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
176      355                      360                      365
177 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
178      370                      375                      380
179 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
180 385                      390                      395                      400
181 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
182      405                      410                      415
183 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
184      420                      425                      430
185 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro

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186          435          440          445
187 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
188          450          455          460
189 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
190 465          470          475          480
191 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His
192          485          490          495
193 Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
194          500          505          510
195 Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
196          515          520          525
197 Thr Pro Asn Tyr Leu Tyr Asn Ser Asp Gly Asn Leu Ala Thr Arg Pro
198          530          535          540
199 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
200 545          550          555          560
201 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
202          565          570          575
203 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
204          580          585          590
205 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
206          595          600          605
207 Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
208          610          615          620
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210 625          630          635
212 <210> SEQ ID NO: 11
213 <211> LENGTH: 639
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Mutant 9.16.6C11 (V494A, C515S) of D. dendroides
219 GaO
221 <400> SEQUENCE: 11
222 Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
223 1          5          10          15
224 Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
225          20          25          30
226 Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
227          35          40          45
228 Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
229          50          55          60
230 Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
231 65          70          75          80
232 Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
233          85          90          95
234 Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
235          100          105          110
236 Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
237          115          120          125

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238 Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
239      130      135      140
240 Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
241 145      150      155      160
242 Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile
243      165      170      175
244 Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
245      180      185      190
246 Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
247      195      200      205
248 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
249      210      215      220
250 Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
251 225      230      235      240
252 Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
253      245      250      255
254 Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
255      260      265      270
256 Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
257      275      280      285
258 Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
259      290      295      300
260 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
261 305      310      315      320
262 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
263      325      330      335
264 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
265      340      345      350
266 Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
267      355      360      365
268 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
269      370      375      380
270 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
271 385      390      395      400
272 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
273      405      410      415
274 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
275      420      425      430
276 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
277      435      440      445
278 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
279      450      455      460
280 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
281 465      470      475      480
282 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His
283      485      490      495
284 Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
285      500      505      510
286 Gly Leu Ser Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe

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VERIFICATION SUMMARY

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L:1287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28